

What is claimed is:

1. An isolated polynucleotide from coryneform bacteria, comprising a polynucleotide sequence which codes for the sigE gene, chosen from the group consisting of
 - 5 a) polynucleotide which is identical to the extent of at least 70% to a polynucleotide which codes for a polypeptide which comprises the amino acid sequence of SEQ ID No. 2,
 - 10 b) polynucleotide which codes for a polypeptide which comprises an amino acid sequence which is identical to the extent of at least 70% to the amino acid sequence of SEQ ID No. 2,
 - c) polynucleotide which is complementary to the polynucleotides of a) or b), and
 - 15 d) polynucleotide comprising at least 15 successive nucleotides of the polynucleotide sequence of a), b) or c),the polypeptide preferably having the activity of sigma factor E.
- 20 2. A polynucleotide as claimed in claim 1, wherein the polynucleotide is a preferably recombinant DNA which is capable of replication in coryneform bacteria.
3. A polynucleotide as claimed in claim 1, wherein the polynucleotide is an RNA.
- 25 4. A polynucleotide as claimed in claim 2, comprising the nucleic acid sequence as shown in SEQ ID No. 1.
5. A DNA as claimed in claim 2 which is capable of replication, comprising

- (i) the nucleotide sequence shown in SEQ ID No. 1,
or
- (ii) at least one sequence which corresponds to
sequence (i) within the range of the
degeneration of the genetic code, or
- (iii) at least one sequence which hybridizes with the
sequence complementary to sequence (i) or (ii),
and optionally
- (iv) sense mutations of neutral function in (i).
- 10 6. A polynucleotide sequence as claimed in claim 2, which
codes for a polypeptide which comprises the amino acid
sequences shown in SEQ ID No. 2.
7. A coryneform bacterium in which the sigE gene is
enhanced, in particular over-expressed.
- 15 8. The shuttle vector pEC-T18mob2sigEexp, which
- 8.1. comprises a DNA fragment 1930 bp in size which
carries the sigE gene,
- 8.2 the restriction map of which is reproduced in
figure 2, and
- 20 8.3 is deposited in strain DSM5715/pEC-T18mob2sigEexp
under no. DSM 14229 at the Deutsche Sammlung für
Mikroorganismen und Zellenkulturen [German
Collection of Microorganisms and Cell Cultures].
- 25 9. A process for the fermentative preparation of L-amino
acids, in particular lysine, which comprises carrying
out the following steps:
- a) fermentation of the coryneform bacteria which
produce the desired L-amino acid and in which at
least the sigE gene or nucleotide sequences which

code for it are enhanced, in particular over-expressed;

- b) concentration of the L-amino acid in the medium or in the cells of the bacteria, and
 - 5 c) isolation of the L-amino acid.
10. A process as claimed in claim 9, wherein bacteria in which further genes of the biosynthesis pathway of the desired L-amino acid are additionally enhanced are employed.
- 10 11. A process as claimed in claim 9, wherein bacteria in which the metabolic pathways which reduce the formation of the desired L-amino acid are at least partly eliminated are employed.
- 15 12. A process as claimed in claim 9, wherein a strain transformed with a plasmid vector is employed, and the plasmid vector carries the nucleotide sequence which codes for the sigE gene.
- 20 13. A process as claimed in claim 9, wherein the expression of the polynucleotide(s) which code(s) for the sigE gene is enhanced, in particular over-expressed.
14. A process as claimed in claim 9, wherein the regulatory properties of the polypeptide (enzyme protein) for which the polynucleotide sigE codes are increased.
- 25 15. A process as claimed in claim 9, wherein for the preparation of L-amino acids, coryneform microorganisms in which at the same time one or more of the genes chosen from the group consisting of
- 15.1 the dapA gene which codes for dihydrodipicolinate synthase,

- 15.2 the gap gene which codes for glyceraldehyde 3-phosphate dehydrogenase,
- 15.3 the tpi gene which codes for triose phosphate isomerase,
- 5 15.4 the pgk gene which codes for 3-phosphoglycerate kinase,
- 15.5 the zwf gene which codes for glucose 6-phosphate dehydrogenase,
- 10 15.6 the pyc gene which codes for pyruvate carboxylase,
- 15.7 the mqo gene which codes for malate-quinone oxidoreductase,
- 15.8 the lysC gene which codes for a feed-back resistant aspartate kinase,
- 15 15.9 the lysE gene which codes for lysine export,
- 15.10 the hom gene which codes for homoserine dehydrogenase
- 20 15.11 the ilvA gene which codes for threonine dehydratase or the ilvA(Fbr) allele which codes for a feed back resistant threonine dehydratase,
- 15.12 the ilvBN gene which codes for acetohydroxy-acid synthase,
- 25 15.13 the ilvD gene which codes for dihydroxy-acid dehydratase,
- 15.14 the zwal gene which codes for the Zwal protein
- is or are enhanced or over-expressed are fermented.

16. A process as claimed in claim 9, wherein for the preparation of L-amino acids, coryneform microorganisms in which at the same time one or more of the genes chosen from the group consisting of

- 5 16.1 the pck gene which codes for phosphoenolpyruvate carboxykinase,
- 16.2 the pgi gene which codes for glucose 6-phosphate isomerase,
- 16.3 the poxB gene which codes for pyruvate oxidase,
- 10 16.4 the zwa2 gene which codes for the Zwa2 protein
- is or are attenuated are fermented.

17. A coryneform bacterium which contains a vector which carries a polynucleotide as claimed in claim 1.

- 15 18. A process as claimed in one or more of the preceding claims, wherein microorganisms of the genus Corynebacterium are employed.

- 20 19. A process for discovering RNA, cDNA and DNA in order to isolate nucleic acids, or polynucleotides or genes which code for sigma factor E or have a high similarity with the sequence of the sigE gene, wherein the polynucleotide comprising the polynucleotide sequences as claimed in claim 1, 2, 3 or 4 is employed as hybridization probes.

- 25 20. A process as claimed in claim 19, wherein the hybridization is carried out under a stringency corresponding to at most 2x SSC.